

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/910,733DATE: 02/17/98
TIME: 09:55:05

INPUT SET: S23457.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANT: COLOTTA, Francesco
6 MUZIO, Marta
7 MANTOVANI, Alberto
8
9 (ii) TITLE OF INVENTION: INTERLEUKIN-1 ANTAGONIST, DNA ENCODING SAME,
10 AND ANTIBODIES THERETO
11
12 (iii) NUMBER OF SEQUENCES: 17
13
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: BROWDY AND NEIMARK
16 (B) STREET: 419 Seventh Street, N.W., Suite 300
17 (C) CITY: Washington
18 (D) STATE: D.C.
19 (E) COUNTRY: USA
20 (F) ZIP: 20004
21
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Floppy disk
24 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27
28 (vi) CURRENT APPLICATION DATA:
29 (A) APPLICATION NUMBER:
30 (B) FILING DATE:
31 (C) CLASSIFICATION:
32
33 (vii) PRIOR APPLICATION DATA:
34 (A) APPLICATION NUMBER: US 08/476,860
35 (B) FILING DATE: 07-JUN-1995
36
37 (vii) PRIOR APPLICATION DATA:
38 (A) APPLICATION NUMBER: IT MI 94 A 002097
39 (B) FILING DATE: 13-OCT-1994
40
41 (viii) ATTORNEY/AGENT INFORMATION:
42 (A) NAME: YUN, Allen C.
43 (B) REGISTRATION NUMBER: 37,971
44 (C) REFERENCE/DOCKET NUMBER: COLOTTA=1A
45
46 (ix) TELECOMMUNICATION INFORMATION:

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47 (A) TELEPHONE: 202-628-5197
48 (B) TELEFAX: 202-737-3528
49
50

51 (2) INFORMATION FOR SEQ ID NO: 1:
52

53 (i) SEQUENCE CHARACTERISTICS:
54 (A) LENGTH: 25 base pairs
55 (B) TYPE: nucleic acid
56 (C) STRANDEDNESS: single
57 (D) TOPOLOGY: linear
58

59 (ii) MOLECULE TYPE: DNA

60 (iii) HYPOTHETICAL: NO
61

62 (ix) FEATURE:

63 (D) OTHER INFORMATION: RT-PCR oligonucleotide named IRA5
64
6566 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
6768 CTGACTTGTA TGAAGAAGGA GGTGG
69

25

70 (2) INFORMATION FOR SEQ ID NO: 2:
71

72 (i) SEQUENCE CHARACTERISTICS:
73 (A) LENGTH: 20 base pairs
74 (B) TYPE: nucleic acid
75 (C) STRANDEDNESS: single
76 (D) TOPOLOGY: linear
77

78 (ii) MOLECULE TYPE: DNA
7980 (iii) HYPOTHETICAL: NO
81

82 (ix) FEATURE:

83 (D) OTHER INFORMATION: RT-PCR oligonucleotide corresponding
84 to 60-79 of B-actin
8586 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
8788 GCGCTCGTCG TCGACAACGG
89

20

90 (2) INFORMATION FOR SEQ ID NO: 3:
91

92 (i) SEQUENCE CHARACTERISTICS:
93 (A) LENGTH: 21 base pairs
94 (B) TYPE: nucleic acid
95 (C) STRANDEDNESS: single
96 (D) TOPOLOGY: linear
97

98 (ii) MOLECULE TYPE: DNA
99

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100 (iii) HYPOTHETICAL: NO
101
102 (ix) FEATURE:
103 (D) OTHER INFORMATION: RT-PCR backward oligonucleotide
104 complementary to 430-449
105
106 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
107
108 GATAGACAAC GTACATGGCT G 21
109
110 (2) INFORMATION FOR SEQ ID NO: 4:
111
112 (i) SEQUENCE CHARACTERISTICS:
113 (A) LENGTH: 87 base pairs
114 (B) TYPE: nucleic acid
115 (C) STRANDEDNESS: single
116 (D) TOPOLOGY: linear
117
118 (ii) MOLECULE TYPE: DNA
119
120 (iii) HYPOTHETICAL: NO
121
122 (ix) FEATURE:
123 (D) OTHER INFORMATION: Sequence of sIL-lra not in common
124
125 (ix) FEATURE:
126 (A) NAME/KEY: CDS
127 (B) LOCATION: 24..86
128
129 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
130
131 GAATTCGGG CTGCAGTCAC AGA ATG GAA ATC TGC AGA GGC CTC CGC AGT 50
132 Met Glu Ile Cys Arg Gly Leu Arg Ser
133 1 5
134
135 CAC CTA ATC ACT CTC CTC CTC TTC CTG TTC CAT TCA G 87
136 His Leu Ile Thr Leu Leu Leu Phe Leu Phe His Ser
137 10 15 20
138
139
140 (2) INFORMATION FOR SEQ ID NO: 5:
141
142 (i) SEQUENCE CHARACTERISTICS:
143 (A) LENGTH: 21 amino acids
144 (B) TYPE: amino acid
145 (D) TOPOLOGY: linear
146
147 (ii) MOLECULE TYPE: protein
148
149 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
150
151 Met Glu Ile Cys Arg Gly Leu Arg Ser His Leu Ile Thr Leu Leu Leu
152 1 5 10 15

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153
154 Phe Leu Phe His Ser
155 20
156
157 (2) INFORMATION FOR SEQ ID NO: 6:
158
159 (i) SEQUENCE CHARACTERISTICS:
160 (A) LENGTH: 42 base pairs
161 (B) TYPE: nucleic acid
162 (C) STRANDEDNESS: single
163 (D) TOPOLOGY: linear
164
165 (ii) MOLECULE TYPE: DNA
166
167 (iii) HYPOTHETICAL: NO
168
169 (ix) FEATURE:
170 (D) OTHER INFORMATION: Sequence of intracellular IL-1ra
171 typeI not in common
172
173 (ix) FEATURE:
174 (A) NAME/KEY: CDS
175 (B) LOCATION: 33..41
176
177 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
178
179 CAGAAGACCT CCTGTCCTAT GAGGCCCTCC CC ATG GCT TTA G 42
180 Met Ala Leu
181 1
182
183
184 (2) INFORMATION FOR SEQ ID NO: 7:
185
186 (i) SEQUENCE CHARACTERISTICS:
187 (A) LENGTH: 105 base pairs
188 (B) TYPE: nucleic acid
189 (C) STRANDEDNESS: single
190 (D) TOPOLOGY: linear
191
192 (ii) MOLECULE TYPE: DNA
193
194 (iii) HYPOTHETICAL: NO
195
196 (ix) FEATURE:
197 (D) OTHER INFORMATION: Sequence of intracellular IL-1ra
198 typeII not in common
199
200 (ix) FEATURE:
201 (A) NAME/KEY: CDS
202 (B) LOCATION: 33..104
203
204 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
205

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206
207 CAGAAGACCT CCTGTCCTAT GAGGCCCTCC CC ATG GCT TTA GCT GAC TTG TAT      53
208                               Met Ala Leu Ala Asp Leu Tyr
209                               1                               5
210
211 GAA GAA GGA GGT GGA GGA GGA GGA GAA GGT GAA GAC AAT GCT GAC TCA      101
212 Glu Glu Gly Gly Gly Gly Gly Gly Gly Glu Gly Glu Asp Asn Ala Asp Ser
213           10                               15                               20
214
215 AAG G      105
216 Lys
217
218
219 (2) INFORMATION FOR SEQ ID NO: 8:
220
221 (i) SEQUENCE CHARACTERISTICS:
222 (A) LENGTH: 24 amino acids
223 (B) TYPE: amino acid
224 (D) TOPOLOGY: linear
225
226 (ii) MOLECULE TYPE: protein
227
228 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
229
230 Met Ala Leu Ala Asp Leu Tyr Glu Glu Gly Gly Gly Gly Gly Glu
231   1           5           10           15
232
233 Gly Glu Asp Asn Ala Asp Ser Lys
234           20
235
236 (2) INFORMATION FOR SEQ ID NO: 9:
237
238 (i) SEQUENCE CHARACTERISTICS:
239 (A) LENGTH: 474 base pairs
240 (B) TYPE: nucleic acid
241 (C) STRANDEDNESS: single
242 (D) TOPOLOGY: linear
243
244 (ii) MOLECULE TYPE: DNA
245
246 (iii) HYPOTHETICAL: NO
247
248 (ix) FEATURE:
249 (D) OTHER INFORMATION: Common IL-1ra sequence; a nucleotide G
250                        was added in the first position, for computer program
251                        reason, in order to encode the first amino acid Glu
252                        and further in order to avoid the creation of a stop
253                        codon in the inner region of the sequence
254
255 (ix) FEATURE:
256 (A) NAME/KEY: CDS
257 (B) LOCATION: 1..468
258

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SEQUENCE VERIFICATION REPORT
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Original Text